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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=16; hr=16; min=49; sec=18; ms=192;]
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Application No: 10534772   Version No: 1.0

Input Set:

Output Set:

Started:	2008-07-16 14:41:20.943
Finished:	2008-07-16 14:41:23.801
Elapsed:	0 hr(s) 0 min(s) 2 sec(s) 858 ms
Total Warnings:	29
Total Errors:	0
No. of SeqIDs Defined:	29
Actual SeqID Count:	29

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

```
            Input Set:


           Output Set:



             Started:   2008-07-16 14:41:20.943
            Finished:   2008-07-16 14:41:23.801
             Elapsed:   0 hr(s) 0 min(s) 2 sec(s) 858 ms
      Total Warnings:   29
        Total Errors:   0
 No. of SeqIDs Defined:   29
  Actual SeqID Count:    29
```

Error code   Error Description

              This error has occured more than 20 times, will not be displayed

<210> 1
<211> 1041
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 1
gactgtggcc ttcccccaga tgtacctaat gcccagccag ctttggaagg ccgtacaagt 60
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaattat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcatgtaat 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gcccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780
acagttcaga aacctaccac agtaaatgtt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaaat gctcaagcaa cacggagtac acctgtttcc 900
aggacaacca agcattttca tgaaacaacc ccaaataaag gaagtggaac cacttcaggt 960
actacccgtc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020
gtaaccatgg gcttgctgac t   1041

<210> 2
<211> 380
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 2
Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
 1   5   10   15
Glu Leu Pro Arg Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
            20   25   30
Trp Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu
        35   40   45
Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys
    50   55   60
Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys
65   70   75   80
Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser
                85   90   95
Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr
            100   105   110
Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys
        115   120   125
Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys
    130   135   140
Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys
145   150   155   160
Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro
                165   170   175
Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly
            180   185   190
Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser
        195   200   205
Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys
    210   215   220
Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp
225   230   235   240
His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe
                245   250   255
Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu
            260   265   270
Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr
        275   280   285
Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro
    290   295   300
Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr
305   310   315   320
Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr
                325   330   335
Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser
            340   345   350
Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly
        355   360   365
Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
    370   375   380

<210> 3
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 3
cagtgctaca actgtcctaa cccaactgct gactgcaaaa cagccgtcaa ttgttcatct   60
gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaag   120
tttgagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaatga gctaacgtac   180
tactgctgca agaaggacct gtgtaacttt aacgaacagc ttgaaaatgg tgggacatcc   240
ttatcagaga aaacagttct tctgctggtg actccatttc tggcagcagc ctggagcctt   300
catccc   306

<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
 1   5   10   15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
            20   25   30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
        35   40   45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
    50   55   60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
65   70   75   80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
                85   90   95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
            100   105   110
Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
        115   120   125

<210> 5
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 5
atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctaccccc   60
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa   120

```
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtgggggccg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaagtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgtggaggtg ggtcgggtgg cggcggatcc 780
gactgtggcc ttcccccaga tgtacctaat gcccagccag ctttggaagg ccgtacaagt 840
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 900
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga gagttctgc 960
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 1020
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 1080
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 1140
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 1200
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 1260
aaattatttg gctcgacttc tagttttttgt cttatttcag gcagctctgt ccagtggagt 1320
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 1380
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcatgtaat 1440
aaaggattca ccatgattgg agagcactct atttattgta ctgtg            1485
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<210> 6

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
    synthetic construct

<400> 6

```
Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1               5                   10                  15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
            20                  25                  30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
        35                  40                  45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
    50                  55                  60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
65                  70                  75                  80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
                85                  90                  95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
            100                 105                 110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
        115                 120                 125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
    130                 135                 140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
145                 150                 155                 160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
                165                 170                 175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
```

```
                180                 185                 190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
        195                 200                 205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
    210                 215                 220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
225                 230                 235                 240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Gly Gly Gly Ser Gly
                245                 250                 255
Gly Gly Gly Ser Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln
                260                 265                 270
Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr
        275                 280                 285
Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser
    290                 295                 300
Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys
305                 310                 315                 320
Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys
                325                 330                 335
Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu
                340                 345                 350
Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys
        355                 360                 365
Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys
    370                 375                 380
Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile
385                 390                 395                 400
Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys
                405                 410                 415
Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile
                420                 425                 430
Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu
        435                 440                 445
Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly
    450                 455                 460
Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn
465                 470                 475                 480
Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val
                485                 490                 495
```

<210> 7
<211> 1002
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 7

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atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctaccccc 60
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa 120
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtggggccg 360
```

```
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg gaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgttcaggag gaggaggttc cctgcagtgc 780
tacaactgtc ctaacccaac tgctgactgc aaaacagccg tcaattgttc atctgatttt 840
gatgcgtgtc tcattaccaa agctgggtta caagtgtata caagtgttg gaagtttgag 900
cattgcaatt caacgacgt cacaacccgc ttgagggaaa atgagctaac gtactactgc 960
tgcaagaagg acctgtgtaa ctttaacgaa cagcttgaaa at 1002
```

<210> 8
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 8

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Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1               5                  10                  15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
            20                  25                  30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
        35                  40                  45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
    50                  55                  60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
65                  70                  75                  80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
                85                  90                  95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
            100                 105                 110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
        115                 120                 125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
    130                 135                 140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
145                 150                 155                 160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
                165                 170                 175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
            180                 185                 190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
        195                 200                 205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
    210                 215                 220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
225                 230                 235                 240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Ser Gly Gly Gly Gly
                245                 250                 255
Ser Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
            260                 265                 270
Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala
```

```
              275                 280                 285
Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe
     290                 295                 300
Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys
305                 310                 315                 320
Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn
                325                 330


<210> 9
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 9
gactgtggcc ttcccccaga tgtacctaat gcccagccag ctttggaagg ccgtacaagt 60
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 3
```